

SEQUENCE LISTING

<110> AKZO Nobel N.V.

<120> Shiga-like toxin vaccine

<130> 2003.006

<160> 4

<170> PatentIn version 3.2

<210> 1

<211> 1325

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(954)

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ttt tct tcg gta tcc tat tcc cag gag ttt acg ata gac ttt tcg act	96
Phe Ser Ser Val Ser Tyr Ser Gln Glu Phe Thr Ile Asp Phe Ser Thr	
20 25 30	

caa caa agt tat gta tct tcg tta aat agt ata cgg aca gtg ata tcg	144
Gln Gln Tyr Val Ser Ser Leu Asn Ser Ile Arg Thr Val Ile Ser	
35 40 45	

acc cct ctt gaa cat ata tct cag gga gct aca tcg gta tcc gtt att	192
Thr Pro Leu Glu His Ile Ser Gln Gly Ala Thr Ser Val Ser Val Ile	
50 55 60	

aat cat aca cca cca gga agt tat att tcc gta ggt ata cga ggg ctt	240
Asn His Thr Pro Pro Gly Ser Tyr Ile Ser Val Gly Ile Arg Gly Leu	
65 70 75 80	

gat gtt tat cag gag cgt ttt gac cat ctt cgt ctg att att gaa cga	288
Asp Val Tyr Gln Glu Arg Phe Asp His Leu Arg Leu Ile Ile Glu Arg	
85 90 95	

aat aat tta tat gtg gct gga ttt gtt aat acg aca aca aat act ttc	336
Asn Asn Leu Tyr Val Ala Gly Phe Val Asn Thr Thr Thr Asn Thr Phe	
100 105 110	

tac aga ttt tca gat ttt gca cat ata tca ttg ccc ggt gtg aca act	384
Tyr Arg Phe Ser Asp Phe Ala His Ile Ser Leu Pro Gly Val Thr Thr	
115 120 125	

att tcc atg aca acg gac agc agt tat acc act ctg caa cgt gtc gca	432
Ile Ser Met Thr Thr Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala	
130 135 140	

gcg ctg gaa cgt tcc gga atg caa atc agt cgt cac tca ctg gtt tca	480
Ala Leu Glu Arg Ser Gly Met Gln Ile Ser Arg His Ser Leu Val Ser	
145 150 155 160	

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tca tat ctg gcg tta atg gag ttc agt ggt aat aca atg acc aga gat	528
Ser Tyr Leu Ala Leu Met Glu Phe Ser Gly Asn Thr Met Thr Arg Asp	
165 170 175	
gca tca aga gca gtt ctg cgt ttt gtc act gtc aca gca gaa gcc tta	576
Ala Ser Arg Ala Val Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu	
180 185 190	
cgg ttc agg caa ata cag aga gaa ttt cgt ctg gca ctg tct gaa act	624
Arg Phe Arg Gln Ile Gln Arg Glu Phe Arg Leu Ala Leu Ser Glu Thr	
195 200 205	
gct cct gtt tat acg atg acg ccg gaa gac gtg gac ctc act ctg aac	672
Ala Pro Val Tyr Thr Met Thr Pro Glu Asp Val Asp Leu Thr Leu Asn	
210 215 220	
tgg ggg aga atc agc aat gtg ctt ccg gag tat cgg gga gag gct ggt	720
Trp Gly Arg Ile Ser Asn Val Leu Pro Glu Tyr Arg Gly Glu Ala Gly	
225 230 235 240	
gtc aga gtg ggg aga ata tcc ttt aat aat ata tca gcg ata ctt ggt	768
Val Arg Val Gly Arg Ile Ser Phe Asn Asn Ile Ser Ala Ile Leu Gly	
245 250 255	
act gtg gcc gtt ata ctg aat tgt gga aat tca tca aga aca atc aca	816
Thr Val Ala Val Ile Leu Asn Cys Gly Asn Ser Ser Arg Thr Ile Thr	
260 265 270	
ggt gat act tgt aat gag gag acc cag aat ctg agc aca ata tat ctc	864
Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu	
275 280 285	
agg gaa tat caa tca aaa gtt aag agg cag ata ttt tca gac tat cag	912
Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln	
290 295 300	
tca gag gtt gac ata tat aac aga att cgg gat gaa tta tga	954
Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu	
305 310 315	
ataaagtaaa atgttatgtt ttatttacgg cgttactatc ctctctatat gcacacggag	1014
ctccccagac tattacagaa ctatgttcgg aatatcgcaa cacacaaata tatacgataa	1074
atgacaagat actatcatat acggaatcga tggcaggcaa aagagaaatg gttatcatta	1134
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Gln Gln Ser Tyr Val Ser Ser	Leu Asn Ser Ile Arg Thr	Val Ile Ser	
	35	40	45
Thr Pro Leu Glu His Ile Ser	Gln Gly Ala Thr Ser Val Ser Val Ile		
	50	55	60
Asn His Thr Pro Pro Gly Ser Tyr Ile Ser	Val Gly Ile Arg Gly Leu		
65	70	75	80
Asp Val Tyr Gln Glu Arg Phe Asp His	Leu Arg Leu Ile Ile Glu Arg		
	85	90	95
Asn Asn Leu Tyr Val Ala Gly Phe Val Asn Thr Thr Thr	Asn Thr Phe		
	100	105	110
Tyr Arg Phe Ser Asp Phe Ala His Ile Ser Leu Pro Gly Val Thr Thr			
	115	120	125
Ile Ser Met Thr Thr Asp Ser Ser Tyr Thr Thr	Leu Gln Arg Val Ala		
	130	135	140
Ala Leu Glu Arg Ser Gly Met Gln Ile Ser Arg His Ser Leu Val Ser			
145	150	155	160
Ser Tyr Leu Ala Leu Met Glu Phe Ser Gly Asn Thr Met Thr Arg Asp			
	165	170	175
Ala Ser Arg Ala Val Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu			
	180	185	190
Arg Phe Arg Gln Ile Gln Arg Glu Phe Arg Leu Ala Leu Ser Glu Thr			
	195	200	205
Ala Pro Val Tyr Thr Met Thr Pro Glu Asp Val Asp Leu Thr Leu Asn			
	210	215	220
Trp Gly Arg Ile Ser Asn Val Leu Pro Glu Tyr Arg Gly Glu Ala Gly			
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Val Arg Val Gly Arg Ile Ser Phe Asn Asn Ile Ser Ala Ile Leu Gly			
	245	250	255

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Thr Val Ala Val Ile Leu Asn Cys Gly Asn Ser Ser Arg Thr Ile Thr
260 265 270

Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu
275 280 285

Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln
290 295 300

Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
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<212> DNA
<213> Escherichia coli

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gtggctggat ttgttaatac gacaacaaat actttctaca gattttcaga ttttgcacat 360
atatcattgc ccggtgtgac aactatctcc atgacaacgg acagcagtta taccactctg 420
caacgtgtcg cagcgtgga acgttccgga atgcaaatca gtcgtcactc actgggttca 480
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gtcagagtgg ggagaatatc cttaataaat atatcagcga tacttggtac tgtggccgtt 780
atactgaatt gtggaaattc atcaagaaca atcacagggt atacttgtaa tgaggagacc 840
cagaatctga gcacaatata tctcagggaa tatcaatcaa aagttaagag gcagatatatt 900
tcagactatc agtcagagggt tgacatatat aacagaattc gggatgaatt atg aat 956
Met Asn
1

aaa gta aaa tgt tat gtt tta ttt acg gcg tta cta tcc tct cta tat 1004
Lys Val Lys Cys Tyr Val Leu Phe Thr Ala Leu Leu Ser Ser Leu Tyr

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5	10	15	
gca cac gga gct ccc cag	act att aca gaa cta	tgt tcg gaa tat cgc	1052
Ala His Gly Ala Pro Gln	Thr Ile Thr Glu Leu	Cys Ser Glu Tyr Arg	
20	25	30	
aac aca caa ata tat acg	ata aat gac aag ata	cta tca tat acg gaa	1100
Asn Thr Gln Ile Tyr Thr	Ile Asn Asp Lys Ile	Leu Ser Tyr Thr Glu	
35	40	45 50	
tcg atg gca ggc aaa aga	gaa atg gtt atc att	aca ttt aag agc ggc	1148
Ser Met Ala Gly Lys Arg	Glu Met Val Ile Ile	Thr Phe Lys Ser Gly	
55	60	65	
gaa aca ttt cag gtc gaa	gtc ccg ggc agt caa	cat ata gac tcc cag	1196
Glu Thr Phe Gln Val Glu	Val Pro Gly Ser Gln	His Ile Asp Ser Gln	
70	75	80	
aaa aaa gcc att gaa agg	atg aag gac aca tta	aga atc aca tat ctg	1244
Lys Lys Ala Ile Glu Arg	Met Lys Asp Thr Leu	Arg Ile Thr Tyr Leu	
85	90	95	
acc gag acc aaa att gat	aaa tta tgt gta tgg	aat aat aaa acc ccc	1292
Thr Glu Thr Lys Ile Asp	Lys Leu Cys Val Trp	Asn Asn Lys Thr Pro	
100	105	110	
aat tca att gcg gca atc	agt atg aaa aac tag		1325
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Leu Tyr Ala His Gly Ala	Pro Gln Thr Ile Thr	Glu Leu Cys Ser Glu	
20	25	30	
Tyr Arg Asn Thr Gln Ile	Tyr Thr Ile Asn Asp	Lys Ile Leu Ser Tyr	
35	40	45	
Thr Glu Ser Met Ala Gly	Lys Arg Glu Met Val	Ile Ile Thr Phe Lys	
50	55	60	
Ser Gly Glu Thr Phe Gln	Val Glu Val Pro Gly	Ser Gln His Ile Asp	
65	70	75 80	
Ser Gln Lys Lys Ala Ile	Glu Arg Met Lys Asp	Thr Leu Arg Ile Thr	
85	90	95	
Tyr Leu Thr Glu Thr Lys	Ile Asp Lys Leu Cys	Val Trp Asn Asn Lys	

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100

105

110

Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Lys Asn
115 120